



crt sequences.ST25
SEQUENCE LISTING

<110> St. Boniface General Hospital Research Centre
Mesaeli, Nasrin
<120> Transgenic Mouse over-expressing calreticulin (CRT) in vascular
smooth muscle cells
<130> 81190-2602
<150> US 60/455399
<151> 2003-03-18
<160> 24
<170> PatentIn version 3.2
<210> 1
<211> 2655
<212> DNA
<213> Artificial
<220>
<223> artificial construct of sm22a promoter and CRT cDNA

<220>
<221> CDS
<222> (1319)..(2653)
<223> CRT coding sequence

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tcctgggtga gactgaccct gcctgagggc tctctccttc cctctctcta ctctttcct 180
ccctctcct ctccctctct ctgtttcctg aggtttccag gattggggat gggactcaga 240
gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca 300
cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac 360
tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg 420
tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggt 480
aggatctttc acgataagga ctattttgaa gggagggagg gtgacactgt cctagtcctc 540
ttaccctagt gtcctccagc cttgccaggc cttaaaccatc cgcccattgt caccgctcta 600
gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga 660
agcataccat acctgtgggc aggatgacct atgttctgcc acgcacttg tagccttgga 720
aaggccactt tgaacctcaa ttttctcaac tgttaaattg ggtggtaact gctatctcat 780
aataaagggg aacgtgaaag gaaggcgttt gcatagtgcc tggttgtgca gccaggctgc 840
agtcaagact agttcccacc aactcgattt taaagccttg caagaagggt gcttgtttgt 900
cccttgacagg ttcctttgtc gggccaaact ctagaatgcc tccccctttc tttctcattg 960

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aagagcagac ccaagtccgg gtaacaagga aggggtttcag ggtcctgccc ataaaagggtt	1020
tttcccggcc gccctcagca ccgccccgcc ccgacccccg cagcatctcc aaagcatgca	1080
gagaatgtct ccggctgccc ccgacagact gctccaactt ggtgtctttc cccaaatatg	1140
gagcctgtgt ggagtgagtg gggcgccccg ggggtggtgag ccaagcagac ttccatgggc	1200
agggagggggc gccagcggac ggcagagggg tgacatcact gcctaggcgg cctttaaacc	1260
cctcacccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggaattc	1318
atg ctg ctc cct gtg ccg ctg ctg ctc ggc ctg ctc ggc ctg gcc gcc Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala 1 5 10 15	1366
gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly 20 25 30	1414
tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys 35 40 45	1462
ttc gtc ctc agt tcg ggc aag ttc tac ggc gat cag gag aaa gat aaa Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys 50 55 60	1510
ggg ctg cag acc agc cag gac gcc cgc ttc tac ggc ctg tcg gcc cga Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Tyr Ala Leu Ser Ala Arg 65 70 75 80	1558
ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala 85 90 95	1606
agg acg ccc gct tct acg ccc tgt cgg ccc gat tcg agc cgt tca gca Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala 100 105 110	1654
aca agg gcc agc cac tgg tgg tgc agt tca ccg tga aac acg agc aga Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro Asn Thr Ser Arg 115 120 125	1702
aca ttg act gcg ggg gcg gct acg tga agc tgt ttc cgg ccg gcc tgg Thr Leu Thr Ala Gly Ala Ala Thr Thr Ser Cys Phe Arg Pro Ala Trp 130 135 140	1750
acc aga agg aca tgc acg ggg act ctg agt aca aca tca tgt ttg gtc Thr Arg Arg Thr Cys Thr Gly Thr Leu Ser Thr Thr Ser Cys Leu Val 145 150 155	1798
ctg aca tct gtg gcc ccg gca cca aga agg ttc acg tca tct tca act Leu Thr Ser Val Ala Pro Ala Pro Arg Arg Phe Thr Ser Ser Ser Thr 160 165 170	1846
aca agg gca aga acg tgc tga tca aca agg aca tcc gtt gca agg acg Thr Arg Ala Arg Thr Cys Ser Ser Thr Arg Thr Ser Val Ala Arg Thr 175 180 185	1894
acg agt tca cac acc tgt aca cgc tga tcg tgc ggc cgg aca aca cgt Thr Ser Ser His Thr Cys Thr Arg Ser Ser Cys Gly Arg Thr Thr Arg 1942	

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190		195		200													
atg	agg	tga	aga	ttg	aca	aca	gcc	agg	tgg	agt	cgg	gct	ccc	tgg	agg		1990
Met	Arg		Arg	Leu	Thr	Thr	Ala	Arg	Trp	Ser	Arg	Ala	Pro	Trp	Arg		
205						210					215						
atg	act	ggg	act	tcc	tac	ccc	cca	aga	aga	taa	agg	acc	cag	atg	cct		2038
Met	Thr	Gly	Thr	Ser	Tyr	Pro	Pro	Arg	Arg		Arg	Thr	Gln	Met	Pro		
220					225						230						
cga	agc	ctg	aag	act	ggg	acg	agc	ggg	cca	aga	tcg	acg	acc	cca	cgg		2086
Arg	Ser	Leu	Lys	Thr	Gly	Thr	Ser	Gly	Pro	Arg	Ser	Thr	Thr	Pro	Arg		
235					240					245					250		
act	cca	agc	ccg	agg	act	ggg	aca	agc	ccg	agc	aca	tcc	ccg	acc	cgg		2134
Thr	Pro	Ser	Pro	Arg	Thr	Gly	Thr	Ser	Pro	Ser	Thr	Ser	Pro	Thr	Arg		
				255					260					265			
acg	cga	aga	agc	ccg	aag	act	ggg	acg	aag	aaa	tgg	acg	gag	agt	ggg		2182
Thr	Arg	Arg	Ser	Pro	Lys	Thr	Gly	Thr	Lys	Lys	Trp	Thr	Glu	Ser	Gly		
			270					275					280				
agc	cgc	cgg	tga	ttc	aga	acc	ccg	agt	aca	agg	gtg	agt	gga	agc	cgc		2230
Ser	Arg	Arg		Phe	Arg	Thr	Pro	Ser	Thr	Arg	Val	Ser	Gly	Ser	Arg		
		285						290					295				
ggc	aga	tcg	aca	acc	ccg	att	aca	aag	gca	cct	gga	tcc	acc	ccg	aaa		2278
Gly	Arg	Ser	Thr	Thr	Pro	Ile	Thr	Lys	Ala	Pro	Gly	Ser	Thr	Pro	Lys		
		300					305					310					
tcg	aca	acc	ccg	agt	act	cgc	ccg	acg	cta	aca	tct	atg	cct	acg	aca		2326
Ser	Thr	Thr	Pro	Ser	Thr	Arg	Pro	Thr	Leu	Thr	Ser	Met	Pro	Thr	Thr		
	315					320					325						
gct	ttg	ccg	tgc	tgg	gct	tgg	acc	tct	ggc	agg	tca	agt	cgg	gca	cca		2374
Ala	Leu	Pro	Cys	Trp	Ala	Trp	Thr	Ser	Gly	Arg	Ser	Ser	Arg	Ala	Pro		
330					335					340					345		
tct	tcg	aca	act	tcc	tca	tca	cca	acg	atg	agg	cgt	acg	cag	agg	agt		2422
Ser	Ser	Thr	Thr	Ser	Ser	Ser	Pro	Thr	Met	Arg	Arg	Thr	Gln	Arg	Ser		
				350					355					360			
ttg	gca	acg	aga	cgt	ggg	gcg	tca	cca	aga	cgg	ccg	aga	agc	aga	tga		2470
Leu	Ala	Thr	Arg	Arg	Gly	Ala	Ser	Pro	Arg	Arg	Pro	Arg	Ser	Arg			
			365					370					375				
aag	aca	agc	agg	acg	agg	agc	agc	gga	tga	agg	agg	agg	agg	agg	aga		2518
Lys	Thr	Ser	Arg	Thr	Arg	Ser	Ser	Gly		Arg	Arg	Arg	Arg	Arg	Arg		
			380					385						390			
aga	agc	gga	agg	agg	agg	agg	agg	ccg	agg	agg	acg	agg	agg	aca	agg		2566
Arg	Ser	Gly	Arg	Arg	Arg	Arg	Arg	Pro	Arg	Arg	Thr	Arg	Arg	Thr	Arg		
			395					400					405				
acg	aca	agg	agg	acg	agg	atg	agg	acg	agg	agg	aca	agg	acg	agg	agg		2614
Thr	Thr	Arg	Arg	Thr	Arg	Met	Arg	Thr	Arg	Arg	Thr	Arg	Thr	Arg	Arg		
		410				415						420					
agg	agg	agg	cgg	ccg	ccg	gcc	agg	cca	agg	acg	agc	tgt	ag		2655		
Arg	Arg	Arg	Arg	Pro	Pro	Ala	Arg	Pro	Arg	Thr	Ser	Cys					
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crt sequences.ST25

<210> 2
 <211> 123
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 2

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
 1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
 20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
 35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
 50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
 65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala
 85 90 95

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala
 100 105 110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro
 115 120

<210> 3
 <211> 12
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 3

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr
 1 5 10

<210> 4
 <211> 45
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

crt sequences.ST25

<400> 4

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu
1 5 10 15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg
20 25 30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys
35 40 45

<210> 5

<211> 17

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 5

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr
1 5 10 15

Arg

<210> 6

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 6

Ser Cys Gly Arg Thr Thr Arg Met Arg
1 5

<210> 7

<211> 23

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 7

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly
1 5 10 15

Thr Ser Tyr Pro Pro Arg Arg
20

crt sequences.ST25

<210> 8
 <211> 56
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 8

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg
 1 5 10 15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser
 20 25 30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys
 35 40 45

Trp Thr Glu Ser Gly Ser Arg Arg
 50 55

<210> 9
 <211> 91
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 9

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr
 1 5 10 15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro
 20 25 30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys
 35 40 45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr
 50 55 60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg
 65 70 75 80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg
 85 90

<210> 10

crt sequences.ST25

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 10

Lys Thr Ser Arg Thr Arg Ser Ser Gly
1 5

<210> 11
<211> 51
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 11

Arg Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg
1 5 10 15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg
20 25 30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Arg Pro Arg
35 40 45

Thr Ser Cys
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<210> 12
<211> 2691
<212> DNA
<213> Artificial

<220>
<223> construct of SM22a promoter and CRT cDNA with HA tag inserted
into CRT cDNA

<220>
<221> CDS
<222> (1319)..(2689)

<220>
<221> misc_feature
<222> (2635)..(2670)
<223> HA insertion

<400> 12
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gccaggctgg ctgtagtgga ttgagcgtct gaggctgcac ctctctggcc tgcagccagt 120

crt sequences.ST25

tcctgggtga gactgaccct gcctgagggg tctctccttc cctctctcta ctcctttcct	180
ccctctccct ctccctctct ctgtttcctg aggtttccag gattggggat gggactcaga	240
gacaccacta aagccttacc ttttaagaag ttgcattcag tgagtgtgtg agacatagca	300
cagatagggg cagaggagag ctggttctgt ctccactgtg tttggtcttg ggtactgaac	360
tcagaccatc aggtgtgata gcagttgtct ttaaccctaa ccctgagcct gtctcacctg	420
tcccttccca agaccactga agctaggtgc aagataagtg gggacccttt ctgaggtggt	480
aggatctttc acgataagga ctattttgaa gggagggagg gtgacactgt cctagtcctc	540
ttaccctagt gtcctccagc cttgccaggc cttaaaccatc cgcccattgt caccgctcta	600
gaaggggcca gggttgactt gctgctaaac aaggcactcc ctagagaagc acccgctaga	660
agcataccat acctgtgggc aggatgaccc atgtttctgcc acgcacttgg tagccttgga	720
aaggccactt tgaacctcaa ttttctcaac tgttaaattg ggtggtaact gctatctcat	780
aataaagggg aacgtgaaag gaaggcgttt gcatagtgcc tggttgtgca gccaggctgc	840
agtcaagact agttcccacc aactcgattt taaagccttg caagaagggtg gcttgtttgt	900
cccttgacagg ttcctttgtc gggccaaact ctagaatgcc tccccctttc tttctcattg	960
aagagcagac ccaagtccgg gtaacaagga agggtttcag ggtcctgccc ataaaagggtt	1020
tttcccggcc gccctcagca ccgccccgcc ccgacccccg cagcatctcc aaagcatgca	1080
gagaatgtct ccggctgccc ccgacagact gctccaactt ggtgtctttc cccaaatatg	1140
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cctcacccag ccggcgcccc accgagctcg gatccactag tccagtgtgg tggaattc	1318
atg ctg ctc cct gtg ccg ctg ctg ctc ggc ctg ctc ggc ctg gcc gcc	1366
Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala	
1 5 10 15	
gcc gag ccc gtc gtc tac ttc aag gag cag ttt ctg gac gga gat ggg	1414
Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly	
20 25 30	
tgg acc gag cgc tgg atc gaa tcc aaa cac aag tcc gat ttt ggc aaa	1462
Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys	
35 40 45	
ttc gtc ctc agt tgc ggc aag ttc tac ggc gat cag gag aaa gat aaa	1510
Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys	
50 55 60	
ggg ctg cag acc agc cag gac gcc cgc ttc tac gcc ctg tgc gcc cga	1558
Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg	
65 70 75 80	
ttc gag ccg ttc agc aac aag ggc cag cca ctg gtg gtg cag cca gcc	1606
Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala	
85 90 95	

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agg Arg	acg Thr	ccc Pro	gct Ala 100	tct Ser	acg Thr	ccc Pro	tgt Cys 105	cgg Arg	ccc Pro	gat Asp	tcg Ser	agc Ser	cgt Arg 110	tca Ser	gca Ala	1654
aca Thr	agg Arg	gcc Ala 115	agc Ser	cac His	tgg Trp	tgg Trp	tgc Cys 120	agt Ser	tca Ser	ccg Pro	tga	aac Asn	acg Thr 125	agc Ser	aga Arg	1702
aca Thr	ttg Leu	act Thr 130	gcg Ala	ggg Gly	gcg Ala	gct Ala	acg Thr 135	tga	agc Ser	tgt Cys	ttc Phe	cgg Arg	ccg Pro 140	gcc Ala	tgg Trp	1750
acc Thr	aga Arg	agg Arg 145	aca Thr	tgc Cys	acg Thr	ggg Gly	act Thr 150	ctg Leu	agt Ser	aca Thr	aca Thr	tca Ser 155	tgt Cys	ttg Leu	gtc Val	1798
ctg Leu 160	aca Thr	tct Ser	gtg Val	gcc Ala	ccg Pro	gca Ala 165	cca Pro	aga Arg	agg Arg	ttc Phe	acg Thr 170	tca Ser	tct Ser	tca Ser	act Thr	1846
aca Thr 175	agg Arg	gca Ala	aga Arg	acg Thr	tgc Cys 180	tga	tca Ser	aca Thr	agg Arg	aca Thr	tcc Ser 185	gtt Val	gca Ala	agg Arg	acg Thr	1894
acg Thr 190	agt Ser	tca Ser	cac His	acc Thr	tgt Cys 195	aca Thr	cgc Arg	tga	tcg Ser	tgc Cys	ggc Gly 200	cgg Arg	aca Thr	aca Thr	cgt Arg	1942
atg Met 205	agg Arg	tga	aga Arg	ttg Leu	aca Thr	aca Thr 210	gcc Ala	agg Arg	tgg Trp	agt Ser	cgg Arg 215	gct Ala	ccc Pro	tgg Trp	agg Arg	1990
atg Met 220	act Thr	ggg Gly	act Thr	tcc Ser	tac Tyr 225	ccc Pro	cca Pro	aga Arg	aga Arg	taa	agg Arg 230	acc Thr	cag Gln	atg Met	cct Pro	2038
cga Arg 235	agc Ser	ctg Leu	aag Lys	act Thr	ggg Gly 240	acg Thr	agc Ser	ggg Gly	cca Pro	aga Arg 245	tcg Ser	acg Thr	acc Thr	cca Pro	cgg Arg 250	2086
act Thr	cca Pro	agc Ser	ccg Pro	agg Arg 255	act Thr	ggg Gly	aca Thr	agc Ser	ccg Pro 260	agc Ser	aca Thr	tcc Ser	ccg Pro	acc Thr 265	cgg Arg	2134
acg Thr	cga Arg	aga Arg	agc Ser 270	ccg Pro	aag Lys	act Thr	ggg Gly	acg Thr 275	aag Lys	aaa Lys	tgg Trp	acg Thr	gag Glu 280	agt Ser	ggg Gly	2182
agc Ser	cgc Arg	cgg Arg 285	tga	ttc Phe	aga Arg	acc Thr	ccg Pro	agt Ser 290	aca Thr	agg Arg	gtg Val	agt Ser	gga Gly 295	agc Ser	cgc Arg	2230
ggc Gly	aga Arg	tcg Ser 300	aca Thr	acc Thr	ccg Pro	att Ile	aca Thr 305	aag Lys	gca Ala	cct Pro	gga Gly 310	tcc Ser	acc Thr	ccg Pro	aaa Lys	2278
tcg Ser	aca Thr 315	acc Thr	ccg Pro	agt Ser	act Thr	cgc Arg 320	ccg Pro	acg Thr	cta Leu	aca Thr	tct Ser 325	atg Met	cct Pro	acg Thr	aca Thr	2326
gct Ala	ttg Leu	ccg Pro	tgc Cys	tgg Trp	gct Ala	tgg Trp	acc Thr	tct Ser	ggc Gly	agg Arg	tca Ser	agt Ser	cgg Arg	gca Ala	cca Pro	2374

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330		335		340		345										
tct	tcg	aca	act	tcc	tca	tca	cca	acg	atg	agg	cgt	acg	cag	agg	agt	2422
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ttg	gca	acg	aga	cgt	ggg	gcg	tca	cca	aga	cgg	ccg	aga	agc	aga	tga	2470
Leu	Ala	Thr	Arg	Arg	Gly	Ala	Ser	Pro	Arg	Arg	Pro	Arg	Ser	Arg		
			365					370					375			
aag	aca	agc	agg	acg	agg	agc	agc	gga	tga	agg	agg	agg	agg	agg	aga	2518
Lys	Thr	Ser	Arg	Thr	Arg	Ser	Ser	Gly		Arg	Arg	Arg	Arg	Arg	Arg	
			380					385						390		
aga	agc	gga	agg	agg	agg	agg	agg	ccg	agg	agg	acg	agg	agg	aca	agg	2566
Arg	Ser	Gly	Arg	Arg	Arg	Arg	Arg	Pro	Arg	Arg	Thr	Arg	Arg	Thr	Arg	
			395					400					405			
acg	aca	agg	agg	acg	agg	atg	agg	acg	agg	agg	aca	agg	acg	agg	agg	2614
Thr	Thr	Arg	Arg	Thr	Arg	Met	Arg	Thr	Arg	Arg	Thr	Arg	Thr	Arg	Arg	
			410				415					420				
agg	agg	agg	cgg	ccg	ccg	gcc	tcg	agt	acc	cat	atg	atg	ttc	ctg	act	2662
Arg	Arg	Arg	Arg	Pro	Pro	Ala	Ser	Ser	Thr	His	Met	Met	Phe	Leu	Thr	
			425			430					435					
atg	cta	gac	agg	cca	agg	acg	agc	tgt	ag							2691
Met	Leu	Asp	Arg	Pro	Arg	Thr	Ser	Cys								
440					445											

<210> 13
 <211> 123
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 13

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
 1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
 20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
 35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
 50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
 65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Pro Ala
 85 90 95

crt sequences.ST25

Arg Thr Pro Ala Ser Thr Pro Cys Arg Pro Asp Ser Ser Arg Ser Ala
 100 105 110

Thr Arg Ala Ser His Trp Trp Cys Ser Ser Pro
 115 120

<210> 14
 <211> 12
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 14

Asn Thr Ser Arg Thr Leu Thr Ala Gly Ala Ala Thr
 1 5 10

<210> 15
 <211> 45
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 15

Ser Cys Phe Arg Pro Ala Trp Thr Arg Arg Thr Cys Thr Gly Thr Leu
 1 5 10 15

Ser Thr Thr Ser Cys Leu Val Leu Thr Ser Val Ala Pro Ala Pro Arg
 20 25 30

Arg Phe Thr Ser Ser Ser Thr Thr Arg Ala Arg Thr Cys
 35 40 45

<210> 16
 <211> 17
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

Ser Thr Arg Thr Ser Val Ala Arg Thr Thr Ser Ser His Thr Cys Thr
 1 5 10 15

Arg

crt sequences.ST25

<210> 17
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 17

Ser Cys Gly Arg Thr Thr Arg Met Arg
 1 5

<210> 18
 <211> 23
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 18

Arg Leu Thr Thr Ala Arg Trp Ser Arg Ala Pro Trp Arg Met Thr Gly
 1 5 10 15

Thr Ser Tyr Pro Pro Arg Arg
 20

<210> 19
 <211> 56
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 19

Arg Thr Gln Met Pro Arg Ser Leu Lys Thr Gly Thr Ser Gly Pro Arg
 1 5 10 15

Ser Thr Thr Pro Arg Thr Pro Ser Pro Arg Thr Gly Thr Ser Pro Ser
 20 25 30

Thr Ser Pro Thr Arg Thr Arg Arg Ser Pro Lys Thr Gly Thr Lys Lys
 35 40 45

Trp Thr Glu Ser Gly Ser Arg Arg
 50 55

<210> 20
 <211> 91
 <212> PRT
 <213> Artificial

crt sequences.ST25

<220>

<223> Synthetic Construct

<400> 20

Phe Arg Thr Pro Ser Thr Arg Val Ser Gly Ser Arg Gly Arg Ser Thr
1 5 10 15

Thr Pro Ile Thr Lys Ala Pro Gly Ser Thr Pro Lys Ser Thr Thr Pro
20 25 30

Ser Thr Arg Pro Thr Leu Thr Ser Met Pro Thr Thr Ala Leu Pro Cys
35 40 45

Trp Ala Trp Thr Ser Gly Arg Ser Ser Arg Ala Pro Ser Ser Thr Thr
50 55 60

Ser Ser Ser Pro Thr Met Arg Arg Thr Gln Arg Ser Leu Ala Thr Arg
65 70 75 80

Arg Gly Ala Ser Pro Arg Arg Pro Arg Ser Arg
85 90

<210> 21

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 21

Lys Thr Ser Arg Thr Arg Ser Ser Gly
1 5

<210> 22

<211> 63

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 22

Arg Arg Arg Arg Arg Arg Arg Ser Gly Arg Arg Arg Arg Arg Pro Arg
1 5 10 15

Arg Thr Arg Arg Thr Arg Thr Thr Arg Arg Thr Arg Met Arg Thr Arg
20 25 30

Arg Thr Arg Thr Arg Arg Arg Arg Arg Arg Pro Pro Ala Ser Ser Thr
Page 13

crt sequences.ST25

35

40

45

His Met Met Phe Leu Thr Met Leu Asp Arg Pro Arg Thr Ser Cys
50 55 60

<210> 23
<211> 418
<212> PRT
<213> Artificial

<220>
<223> CRT peptide sequence from CRT cDNA

<400> 23

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr
85 90 95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
100 105 110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr
115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
130 135 140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
180 185 190

crt sequences.ST25

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn
290 295 300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
355 360 365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu
370 375 380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu
385 390 395 400

Asp Lys Asp Glu Glu Glu Glu Glu Ala Ala Ala Gly Gln Ala Lys Asp
405 410 415

Glu Leu

crt sequences.ST25

<211> 430
 <212> PRT
 <213> Artificial

<220>
 <223> CRT peptide sequence with HA tag inserted into peptide

<220>
 <221> MISC_FEATURE
 <222> (413)..(424)
 <223> HA Tag

<400> 24

Met Leu Leu Pro Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
 1 5 10 15

Ala Glu Pro Val Val Tyr Phe Lys Glu Gln Phe Leu Asp Gly Asp Gly
 20 25 30

Trp Thr Glu Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
 35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Gln Glu Lys Asp Lys
 50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Arg
 65 70 75 80

Phe Glu Pro Phe Ser Asn Lys Gly Gln Pro Leu Val Val Gln Phe Thr
 85 90 95

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
 100 105 110

Phe Pro Ala Gly Leu Asp Gln Lys Asp Met His Gly Asp Ser Glu Tyr
 115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
 130 135 140

His Val Ile Phe Asn Tyr Lys Gly Lys Asn Val Leu Ile Asn Lys Asp
 145 150 155 160

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
 165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
 180 185 190

crt sequences.ST25

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu
225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Ala Asn
290 295 300

Ile Tyr Ala Tyr Asp Ser Phe Ala Val Leu Gly Leu Asp Leu Trp Gln
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Thr
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
355 360 365

Glu Glu Glu Glu Glu Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Glu
370 375 380

Asp Glu Glu Asp Lys Asp Asp Lys Glu Asp Glu Asp Glu Asp Glu Glu
385 390 395 400

Asp Lys Asp Glu Glu Glu Glu Glu Ala Ala Ala Gly Leu Glu Tyr Pro
405 410 415

Tyr Asp Val Pro Asp Tyr Ala Arg Gln Ala Lys Asp Glu Leu
420 425 430